

The Matlab Code to evaluate a single cell time evolution is composed by 7 files.

SingleCell.m

In the script the user can set different Whi5 phosphorylation configurations.

Moreover, we call:

- the function to generate the matrices for the probability distributions of the different phosphorylation states (generate_matrices.m);
- the function to start the simulation (d1_one_cell.m);
- the function to generate the figures (Figures.m).

Besides the time course of all the molecular players involved, as well as of the gene activation curve, the outputs that we provide are:

- T1, T2 and TG1 duration values
- Hill coefficient and Median point values for the Hill function that best fits the fraction of the activated genes
- Protein content at the end of G1 (critical size P_s) and volume at the end of T1 (V_s)
- Linear growth rate α

d1_one_cell.m

In this function, we define:

- all the model parameters;
- the initial conditions;
- the while loop that updates Euler integration step until the condition to exit G1-phase is fulfilled
- the control to define the cell phase

The while loop makes the call to der_plugin.m, a function implementing the ODEs

der_plugin.m

In this function, we define:

- ordinary differential equations of the model that describe the evolution of a cell in the G1/S period.

Figures.m

This function allows to generate the most significant figures presented in the paper. In particular, we plot the evolution of:

- Swi6, Swi4, free unbound Whi5, Swi6Swi4, Swi6Swi4Whi5

- Swi6, Mbp1, Swi6Mbp1
- free Whi5 in the nucleus and Whi5 in the cytoplasm
- Clb5 plus Clb6, Sic1 in the nucleus, Clb5Sic1 +Clb6Sic1, Clb5Sic1p +Clb6Sic1p, Sic1p, Sic1 in the cytoplasm
- Clb5, Clb6, Nrm1, Cln1, Cln2
- Percentage of activated genes and percentage of nuclear Whi5
- Cln2, free Sic1, Clb5, percentage of activated genes

generate_matrices.m

Function that provides the matrices for the probability distributions of the different phosphorylation states.

Best_Hill.m and **Loss_Hill.m**

Functions to evaluate the hill coefficient and the median point for the fraction of G1/S regulon activated genes

RUN THE CODE

To execute the Matlab code, the SingleCell.m script must be run.

```
>>SingleCell
```